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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02 ; Search time 3283 Seconds
                                              (without alignments)
                                              10209.126 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatactttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1 4494.2 100.0   4523 12 AD032292   Ado32292 Bacterial

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02 ; Search time 15 Seconds
                                        (without alignments)
                                        10209.126 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query
   No.   Score   Match Length DB   ID   Description
   ----
     1   18.8   100.0   20   12   ADO32297   Ado32297 Bacterial

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02 ; Search time 17 Seconds
                                            (without alignments)
                                            10209.126 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22.2	100.0	23	12	ADO32340	Ado32340 Bacterial

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02 ; Search time 515 Seconds
                                        (without alignments)
                                    10209.126 Million cell updates/sec

Title: US-10-529-319-8
Perfect score: 709
Sequence: 1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709

Scoring table: IDENTITY_NUCDX
               Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_200701:*
               1: · geneseqn1980s:*
               2: geneseqn1990s:*
               3: geneseqn2000s:*
               4: geneseqn2001as:*
               5: geneseqn2001bs:*
               6: geneseqn2002as:*
               7: geneseqn2002bs:*
               8: geneseqn2003as:*
               9: geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*
               15: geneseqn2006s:*
               16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   709 100.0   709 12   ADO32299   Ado32299 Bacterial

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55 ; Search time 29158 Seconds
                                           (without alignments)
                                 10721.919 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatacttttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1 4494.2 100.0 4523 2   CQ816375   CQ816375 Sequence
     2 4187.4   93.2 4498 15 AF535183   AF535183 Streptoco

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55 ; Search time 129 Seconds
                                            (without alignments)
                                            10721.919 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
       1   18.8   100.0   20   2 CQ816380   CQ816380 Sequence
       2   18.8   100.0   763   2 AX414438   AX414438 Sequence

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55 ; Search time 148 Seconds
                                              (without alignments)
                                              10721.919 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                          %
Result   Query
   No.   Score Match Length DB   ID   Description
        ----
     1   22.2 100.0   23   2   CQ816381   CQ816381 Sequence
     2   22.2 100.0   23   2   CQ816423   CQ816423 Sequence

```
                      GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on:           November  7, 2007, 02:12:55 ; Search time 4571 Seconds
                                              (without alignments)
                                     10721.919 Million cell updates/sec


Title:            US-10-529-319-8
Perfect score:    709
Sequence:         1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709


Scoring table:    IDENTITY_NUCDX
                  Gapop 10.0 , Gapext 1.0


Searched:         7568541 seqs, 34560148153 residues


Total number of hits satisfying chosen parameters:      15137082


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        GenEmbl:*
                  1:  gb_env:*
                  2:  gb_pat:*
                  3:  gb_ph:*
                  4:  gb_pl:*
                  5:  gb_pr:*
                  6:  gb_ro:*
                  7:  gb_sts:*
                  8:  gb_sy:*
                  9:  gb_un:*
                  10:  gb_vi:*
                  11:  gb_ov:*
                  12:  gb_htg:*
                  13:  gb_in:*
                  14:  gb_om:*
                  15:  gb_ba:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES
                      %
Result              Query
   No.    Score   Match Length DB   ID                     Description
--------------------------------------------------------------------------------
     1     709   100.0    709   2   CQ816382              CQ816382 Sequence
     2     693    97.7    693  15   AF535171              AF535171 Streptoco
```

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04 ; Search time 17684 Seconds
                                              (without alignments)
                                              15868.232 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatacttttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	1327	29.5	2768	16	BH770908	BH770908 LLMGtag64
	2	295.2	6.6	3228	17	CL955048	CL955048 OsJRUA000
c	3	280	6.2	1037	18	DU758598	DU758598 ASNG2002.
	4	262	5.8	1026	18	DU780806	DU780806 ASXB3401.
c	5	254.2	5.7	979	18	DU742577	DU742577 ASNC1288.
c	6	239.4	5.3	1021	18	DU739640	DU739640 APKI5317.
c	7	235.2	5.2	721	16	BZ560602	BZ560602 pacs2-164
	8	233.2	5.2	1014	18	DU762284	DU762284 ASNG4109.
	9	228.8	5.1	1009	18	DU761500	DU761500 ASNG3728.
	10	222.8	5.0	682	19	AG275418	AG275418 Cyanidios
	11	217	4.8	988	18	DU766745	DU766745 ANIW13628
c	12	216.2	4.8	1044	18	DU776982	DU776982 ASXB1422.
	13	214	4.8	590	19	AG947952	AG947952 Drosophil
	14	213.2	4.7	527	19	AG947500	AG947500 Drosophil
	15	212.8	4.7	696	19	AG939210	AG939210 Drosophil
	16	210.2	4.7	1204	18	ED033682	ED033682 L001_PA_0
	17	200.8	4.5	614	19	AG935813	AG935813 Drosophil
c	18	197	4.4	652	15	AQ990247	AQ990247 Rfc00983
	19	197	4.4	1143	16	BZ579071	BZ579071 msh2_6169
	20	196.4	4.4	737	19	AG270164	AG270164 Cyanidios
	21	195.2	4.3	589	19	AG946673	AG946673 Drosophil
c	22	194.4	4.3	936	18	DU774013	DU774013 APKG3751.
c	23	191.6	4.3	887	18	DU769412	DU769412 APKG1440.
c	24	188	4.2	783	17	CL686610	CL686610 PRI0144c_
c	25	183.4	4.1	970	18	DU748280	DU748280 ASNC438.b
	26	180.6	4.0	631	16	BH861083	BH861083 H3E3T7 We
c	27	180.2	4.0	633	17	CG896388	CG896388 pastbac02
	28	180.2	4.0	864	18	DU732525	DU732525 APKI1776.
	29	180	4.0	777	13	DN257460	DN257460 Meso09815
c	30	179.6	4.0	929	18	DU750813	DU750813 ASNF1671.
	31	179.2	4.0	712	17	CG896362	CG896362 pastbac02
	32	178.6	4.0	837	2	BG302377	BG302377 IR1-500-2
c	33	177.4	3.9	963	18	DU782014	DU782014 ASXB4014.
	34	176	3.9	528	19	AG269216	AG269216 Cyanidios
c	35	175.4	3.9	1067	18	DU758748	DU758748 ASNG2090.
c	36	175.2	3.9	1017	18	DU749209	DU749209 ASNC950.b
c	37	174.8	3.9	1013	18	DU782058	DU782058 ASXB4036.
	38	174.4	3.9	617	17	CG896695	CG896695 pastbac03
c	39	174.4	3.9	799	18	CZ533942	CZ533942 SRAA-aac8
c	40	172.6	3.8	540	19	AG268676	AG268676 Cyanidios
c	41	172.6	3.8	541	19	AG269121	AG269121 Cyanidios
c	42	172.4	3.8	520	17	CG896610	CG896610 pastbac03
c	43	170.4	3.8	868	18	DU787960	DU787960 APKH2385.
	44	170.4	3.8	908	18	DU732151	DU732151 APKI1587.
c	45	168.2	3.7	880	19	DE245534	DE245534 Trifolium

ALIGNMENTS

RESULT 1
BH770908
LOCUS   BH770908   2768 bp   DNA   linear   GSS 01-MAY-2002
DEFINITION   LLMGtag640 MG1363 Random Sequence Tag Library Lactococcus lactis
             subsp. cremoris genomic, genomic survey sequence.

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04 ; Search time 78 Seconds
                                      (without alignments)
                                      15868.232 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                    %
Result   Query

No.	Score	Match	Length	DB	ID		Description
	1	18.8	100.0	224	2	BE449580	BE449580 EST356339
	2	18.8	100.0	249	17	CG616364	CG616364 OST308403
	3	18.8	100.0	267	2	BG096334	BG096334 EST460853
	4	18.8	100.0	432	4	BQ111873	BQ111873 EST597449
c	5	18.8	100.0	449	15	AQ339001	AQ339001 HS_5021_A
c	6	18.8	100.0	736	1	AI148550	AI148550 qc68f11.x
	7	18.8	100.0	780	12	EB442713	EB442713 KN6B.114O
	8	18.8	100.0	2768	16	BH770908	BH770908 LLMGtag64
	9	17.8	94.7	272	7	BB253849	BB253849 BB253849
	10	17.8	94.7	477	4	BP497438	BP497438 BP497438
	11	17.8	94.7	567	18	DU453884	DU453884 109841577
	12	17.8	94.7	615	10	CR448915	CR448915 CR448915
c	13	17.8	94.7	671	10	CR789429	CR789429 DKFZp459A
	14	17.8	94.7	683	13	DT019698	DT019698 VVI052C01
	15	17.8	94.7	694	9	CN603922	CN603922 USDA_FP_1
	16	17.8	94.7	707	13	DT944068	DT944068 ZM_BFb013
c	17	17.8	94.7	707	13	DV541894	DV541894 ZM_BFb023
	18	17.8	94.7	708	12	EC353178	EC353178 LIVERF091
c	19	17.8	94.7	742	4	BU244836	BU244836 603781034
	20	17.8	94.7	757	13	DR794581	DR794581 ZM_BFb001
c	21	17.8	94.7	775	15	BH562959	BH562959 BOGSU18TF
c	22	17.8	94.7	776	12	EB529281	EB529281 304015 Pi
	23	17.8	94.7	1093	19	CNS05GHC	AL336297 Tetraodon
	24	17.8	94.7	1114	17	CL107680	CL107680 ISB1-48K1
c	25	17.8	94.7	1215	13	DN732200	DN732200 CNB63-A03
c	26	17.8	94.7	2478	6	AY105902	AY105902 Zea mays
	27	17.6	93.6	398	5	BY615872	BY615872 BY615872
	28	17.6	93.6	549	13	DT672330	DT672330 s13dLT33D
	29	17.6	93.6	572	13	DT670519	DT670519 s13dLT55A
	30	17.6	93.6	610	9	CN556183	CN556183 tae21f09.
	31	17.6	93.6	683	13	DN603186	DN603186 ACAC-aab7
c	32	17.6	93.6	754	17	CG922594	CG922594 MBEHD01TR
	33	17.6	93.6	838	16	CC856069	CC856069 NDL.17I6.
c	34	17.6	93.6	970	18	DU748280	DU748280 ASNC438.b
	35	17.4	92.6	813	19	CNS0128M	AL101248 Drosophil
c	36	17.2	91.5	154	2	BE090751	BE090751 PM1-BT072
	37	17.2	91.5	160	17	CE706071	CE706071 tigr-gss-
	38	17.2	91.5	179	2	BE181608	BE181608 CM3-HT063
c	39	17.2	91.5	202	7	AV009565	AV009565 AV009565
	40	17.2	91.5	220	17	CG989474	CG989474 CH240_146
c	41	17.2	91.5	221	15	AZ577061	AZ577061 03e09_Sho
c	42	17.2	91.5	228	7	AW902966	AW902966 CM2-NN102
c	43	17.2	91.5	229	4	BQ353634	BQ353634 CM0-HT091
	44	17.2	91.5	240	11	F36208	F36208 HSPD33600 H
	45	17.2	91.5	242	7	BB571249	BB571249 BB571249

ALIGNMENTS

RESULT 1
BE449580
LOCUS   BE449580   224 bp   mRNA   linear   EST 18-MAY-2001
DEFINITION   EST356339 L. hirsutum trichome, Cornell University Lycopersicon
             hirsutum cDNA clone cLHT32E5, mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04 ; Search time 90 Seconds
                                        (without alignments)
                                        15868.232 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                1: gb_est1:*
                2: gb_est3:*
                3: gb_est4:*
                4: gb_est5:*
                5: gb_est6:*
                6: gb_htc:*
                7: gb_est2:*
                8: gb_est7:*
                9: gb_est8:*
                10: gb_est9:*
                11: gb_est13:*
                12: gb_est12:*
                13: gb_est11:*
                14: gb_est10:*
                15: gb_gss1:*
                16: gb_gss2:*
                17: gb_gss3:*
                18: gb_gss4:*
                19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                        %
Result   Query

	No.	Score	Match	Length	DB	ID	Description
	1	21	94.6	585	4	BP913877	BP913877 BP913877
c	2	21	94.6	642	12	DV678823	DV678823 CGN-16763
c	3	21	94.6	703	12	DV684110	DV684110 CGN-24878
c	4	21	94.6	1318	12	DY280319	DY280319 ICOAAA50D
	5	19.6	88.3	491	3	BI515928	BI515928 BB160020B
c	6	19.6	88.3	734	19	AG443773	AG443773 Mus muscu
c	7	19.6	88.3	756	19	AG561751	AG561751 Mus muscu
c	8	19.4	87.4	275	13	DR973410	DR973410 CHUT007G0
c	9	19.4	87.4	287	7	AW330550	AW330550 ME000718.
	10	19.4	87.4	363	1	AM157805	AM157805 AM157805
c	11	19.4	87.4	405	8	CA969170	CA969170 CcLX06a21
	12	19.4	87.4	426	1	AJ742017	AJ742017 AJ742017
	13	19.4	87.4	429	13	DR973517	DR973517 CHUT007G0
c	14	19.4	87.4	447	9	CN770050	CN770050 taf75a07.
c	15	19.4	87.4	458	4	BP708478	BP708478 BP708478
c	16	19.4	87.4	466	11	EE281162	EE281162 SAAH-aaa9
c	17	19.4	87.4	488	1	AL672625	AL672625 AL672625
c	18	19.4	87.4	493	15	AZ929806	AZ929806 479.dil55
c	19	19.4	87.4	512	4	BU400948	BU400948 603481242
	20	19.4	87.4	512	19	DE064460	DE064460 Oryzias 1
c	21	19.4	87.4	516	4	BU213745	BU213745 603755390
c	22	19.4	87.4	516	15	AZ928670	AZ928670 479.dif14
	23	19.4	87.4	523	19	DE269617	DE269617 Oryzias 1
c	24	19.4	87.4	527	19	AG947500	AG947500 Drosophil
c	25	19.4	87.4	531	4	BU405749	BU405749 603484421
	26	19.4	87.4	536	12	EC386480	EC386480 SAAG-aaa0
c	27	19.4	87.4	540	13	DT693234	DT693234 s13dFA25C
	28	19.4	87.4	542	14	CX457104	CX457104 JGI_XZG54
c	29	19.4	87.4	545	4	BU278033	BU278033 603867034
c	30	19.4	87.4	548	13	DT677406	DT677406 s13dFA51D
c	31	19.4	87.4	548	13	DT677502	DT677502 s13dFA53E
c	32	19.4	87.4	548	13	DT677892	DT677892 s13dFA46E
c	33	19.4	87.4	549	4	BU358974	BU358974 603476958
	34	19.4	87.4	550	12	EC386479	EC386479 SAAG-aaa0
c	35	19.4	87.4	550	13	DT675375	DT675375 s13dFA21C
c	36	19.4	87.4	550	13	DT675647	DT675647 s13dFA23G
c	37	19.4	87.4	555	13	DT710379	DT710379 s13dFA45H
c	38	19.4	87.4	561	7	AW641732	AW641732 cm10f10.w
c	39	19.4	87.4	568	9	CN120035	CN120035 ECOCAA003
c	40	19.4	87.4	572	1	AJ394922	AJ394922 AJ394922
	41	19.4	87.4	573	1	AJ742016	AJ742016 AJ742016
c	42	19.4	87.4	576	4	BU415732	BU415732 603669259
c	43	19.4	87.4	576	5	BY922570	BY922570 BY922570
	44	19.4	87.4	584	9	CN565309	CN565309 tag23e11.
	45	19.4	87.4	584	10	CV671939	CV671939 RE-3-SJ-L

ALIGNMENTS

RESULT 1
BP913877
LOCUS   BP913877   585 bp   mRNA   linear   EST 09-JUN-2005
DEFINITION   BP913877 Adiantum capillus-veneris prothallium Adiantum
             capillus-veneris cDNA clone YMU001_000037_D03, mRNA sequence.

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04 ; Search time 2772 Seconds

(without alignments)

15868.232 Million cell updates/sec

Title: US-10-529-319-8

Perfect score: 709

Sequence: 1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709

Scoring table: IDENTITY_NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :   EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_htc:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_est13:*

12: gb_est12:*

13: gb_est11:*

14: gb_est10:*

15: gb_gss1:*

16: gb_gss2:*

17: gb_gss3:*

18: gb_gss4:*

19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	353	49.8	2768	16	BH770908	BH770908 LLMGtag64
2	255.6	36.1	988	18	DU766745	DU766745 ANIW13628
c 3	168	23.7	473	19	AG267037	AG267037 Cyanidios
c 4	161.4	22.8	1037	18	DU758598	DU758598 ASNG2002.
c 5	157.6	22.2	451	19	AG269635	AG269635 Cyanidios
c 6	146.2	20.6	954	18	DU795369	DU795369 APKH590.b
7	140.2	19.8	476	19	AG273937	AG273937 Cyanidios
c 8	139.8	19.7	397	19	AG267808	AG267808 Cyanidios
9	136.6	19.3	587	15	BH382180	BH382180 AG-ND-105
c 10	133.6	18.8	683	15	AQ367283	AQ367283 toxb0002l
11	128.8	18.2	759	17	CG026988	CG026988 PGAAC15TR
c 12	128.6	18.1	551	16	BZ957712	BZ957712 PgH006O15
c 13	127.4	18.0	969	18	DU739459	DU739459 APKI5174.
c 14	126	17.8	716	17	CW441245	CW441245 fsbb001f1
c 15	125.6	17.7	540	19	AG268676	AG268676 Cyanidios

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:31:22 ; Search time 1037 Seconds
                                       (without alignments)
                                       16344.423 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatactttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: · 10310350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
                2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
                3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
                4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
                5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
                6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
                7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
                8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
                9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
                10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
                11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	2898	64.5	14672	3	US-08-961-527-111	Sequence 111, App
c 2	2898	64.5	14672	5	US-10-158-844-111	Sequence 111, App
3	2470.4	55.0	3651	3	US-09-107-433-1652	Sequence 1652, Ap
4	2467.2	54.9	3612	3	US-09-583-110-973	Sequence 973, App
5	2467.2	54.9	3612	5	US-11-028-099A-973	Sequence 973, App
6	2467.2	54.9	3612	5	US-11-028-291A-973	Sequence 973, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12 ; Search time 52 Seconds
                                        (without alignments)
                                        9152.710 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
                 17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
                 18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
                 19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*
                 20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*
                 21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*
                 22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
                 23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*
                 24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*
                 25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*
                 26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*
                 27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.8	100.0	20	14	US-10-529-319-6	Sequence 6, Appli
c	2	18.8	100.0	162	3	US-09-815-242-992	Sequence 992, App
c	3	18.8	100.0	162	9	US-10-282-122A-977	Sequence 977, App
c	4	18.8	100.0	456	3	US-09-815-242-3096	Sequence 3096, Ap
c	5	18.8	100.0	456	9	US-10-282-122A-5649	Sequence 5649, Ap
	6	18.8	100.0	763	9	US-10-398-221-1429	Sequence 1429, Ap
	7	18.8	100.0	891	11	US-10-750-185-42683	Sequence 42683, A
	8	18.8	100.0	891	11	US-10-750-623-42683	Sequence 42683, A
	9	18.8	100.0	891	15	US-10-750-622-42683	Sequence 42683, A
	10	18.8	100.0	2205	14	US-10-434-665-2197	Sequence 2197, Ap
	11	18.8	100.0	3096	14	US-10-529-319-5	Sequence 5, Appli
	12	18.8	100.0	3198	14	US-10-529-319-4	Sequence 4, Appli
	13	18.8	100.0	3405	9	US-10-282-122A-35573	Sequence 35573, A
	14	18.8	100.0	3411	3	US-09-815-242-8349	Sequence 8349, Ap
	15	18.8	100.0	3411	3	US-09-815-242-8716	Sequence 8716, Ap
	16	18.8	100.0	3425	14	US-10-529-319-3	Sequence 3, Appli
	17	18.8	100.0	3474	3	US-09-815-242-3939	Sequence 3939, Ap
	18	18.8	100.0	3537	3	US-09-815-242-4467	Sequence 4467, Ap
	19	18.8	100.0	3549	10	US-10-470-048B-125	Sequence 125, App
	20	18.8	100.0	3549	13	US-10-471-571A-3397	Sequence 3397, Ap
	21	18.8	100.0	3552	9	US-10-282-122A-7607	Sequence 7607, Ap
	22	18.8	100.0	3552	10	US-10-857-625-235	Sequence 235, App
	23	18.8	100.0	3552	15	US-10-859-198-1712	Sequence 1712, Ap
	24	18.8	100.0	3552	15	US-10-859-198-9564	Sequence 9564, Ap
	25	18.8	100.0	3555	9	US-10-282-122A-24519	Sequence 24519, A
	26	18.8	100.0	3561	9	US-10-282-122A-36012	Sequence 36012, A
	27	18.8	100.0	3564	22	US-11-434-137-379	Sequence 379, App
	28	18.8	100.0	3564	22	US-11-434-184-379	Sequence 379, App
	29	18.8	100.0	3564	22	US-11-434-199-379	Sequence 379, App
	30	18.8	100.0	3564	22	US-11-434-203-379	Sequence 379, App
	31	18.8	100.0	3564	22	US-11-434-127-379	Sequence 379, App
	32	18.8	100.0	3567	9	US-10-282-122A-38159	Sequence 38159, A
	33	18.8	100.0	3567	14	US-10-513-024-723	Sequence 723, App
	34	18.8	100.0	3567	22	US-11-348-413-1550	Sequence 1550, Ap
	35	18.8	100.0	3578	3	US-09-974-300-1310	Sequence 1310, Ap
	36	18.8	100.0	3578	23	US-11-203-606-1310	Sequence 1310, Ap
	37	18.8	100.0	3579	11	US-10-498-302-1	Sequence 1, Appli
	38	18.8	100.0	3582	8	US-10-369-493-46739	Sequence 46739, A
	39	18.8	100.0	3591	8	US-10-369-493-42178	Sequence 42178, A
	40	18.8	100.0	3612	9	US-10-282-122A-6253	Sequence 6253, Ap
	41	18.8	100.0	3624	3	US-09-815-242-6529	Sequence 6529, Ap
	42	18.8	100.0	3624	9	US-10-282-122A-21771	Sequence 21771, A
	43	18.8	100.0	3698	10	US-10-488-588-5	Sequence 5, Appli
	44	18.8	100.0	3791	10	US-10-488-588-3	Sequence 3, Appli
	45	18.8	100.0	3851	10	US-10-488-588-6	Sequence 6, Appli

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:31:22 ; Search time 5 Seconds
                                    (without alignments)
                                    16344.423 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
                2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
                3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
                4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
                5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
                6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
                7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
                8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
                9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
                10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
                11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	22.2	100.0	271	3	US-08-956-171E-4462	Sequence 4462, Ap
c 2	22.2	100.0	271	3	US-08-781-986A-4462	Sequence 4462, Ap
3	22.2	100.0	400	3	US-08-956-171E-4154	Sequence 4154, Ap
4	22.2	100.0	400	3	US-08-781-986A-4154	Sequence 4154, Ap
c 5	22.2	100.0	2205	3	US-09-134-000C-2197	Sequence 2197, Ap
6	22.2	100.0	14672	3	US-08-961-527-111	Sequence 111, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:31:22 ; Search time 162 Seconds
                                   (without alignments)
                                 16344.423 Million cell updates/sec

Title: US-10-529-319-8
Perfect score: 709
Sequence: 1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/ina/7A_COMB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/ina/7B_COMB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/ina/H_COMB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/ina/PCTUS_COMB.seq:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/ina/PP_COMB.seq:*
                 10: /EMC_Celerra_SIDS2/ptodata/1/ina/RE_COMB.seq:*
                 11: /EMC_Celerra_SIDS2/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
  No.   Score Match Length DB ID   Description
----
     1   566.6   79.9   3612   3 US-09-583-110-973   Sequence 973, App
     2   566.6   79.9   3612   5 US-11-028-099A-973   Sequence 973, App
     3   566.6   79.9   3612   5 US-11-028-291A-973   Sequence 973, App
     4   566.6   79.9   3612   5 US-11-027-878A-973   Sequence 973, App
     5   566.6   79.9   3612   5 US-11-027-399-973   Sequence 973, App
     6   566.6   79.9   3612   5 US-11-027-877A-973   Sequence 973, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12 ; Search time 11727 Seconds
                                        (without alignments)
                                        9152.710 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatacttttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
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         15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
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         17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4494.2	100.0	4523	14	US-10-529-319-1	Sequence 1, Appli
c	2	2898	64.5	14672	2	US-08-961-527-111	Sequence 111, App
c	3	2898	64.5	14672	9	US-10-158-844-111	Sequence 111, App
c	4	2898	64.5	14672	27	US-11-563-552-111	Sequence 111, App
c	5	2898	64.5	2162598	10	US-10-472-928-4979	Sequence 4979, Ap
	6	2717	60.5	2160266	14	US-10-513-024-1373	Sequence 1373, Ap
	7	2717	60.5	2160266	22	US-11-434-137-10967	Sequence 10967, A
	8	2717	60.5	2160266	22	US-11-434-184-10967	Sequence 10967, A
	9	2717	60.5	2160266	22	US-11-434-199-10967	Sequence 10967, A
	10	2717	60.5	2160266	22	US-11-434-203-10967	Sequence 10967, A
	11	2717	60.5	2160266	22	US-11-434-127-10967	Sequence 10967, A
	12	2480	55.2	3651	9	US-10-282-122A-37985	Sequence 37985, A
	13	2470.4	55.0	3651	11	US-10-617-320-1652	Sequence 1652, Ap
	14	2467.2	54.9	3612	23	US-11-027-802-973	Sequence 973, App
	15	2467.2	54.9	3612	23	US-11-027-892-973	Sequence 973, App
	16	2467.2	54.9	3612	23	US-11-028-050-973	Sequence 973, App
	17	2467.2	54.9	3612	23	US-11-028-149-973	Sequence 973, App
	18	2467.2	54.9	3612	23	US-11-028-197-973	Sequence 973, App
	19	2467.2	54.9	3612	23	US-11-028-204-973	Sequence 973, App
	20	2467.2	54.9	3612	23	US-11-028-458-973	Sequence 973, App
	21	2467.2	54.9	3612	23	US-11-524-439-973	Sequence 973, App
	22	2467.2	54.9	3612	23	US-11-524-493-973	Sequence 973, App
	23	2467.2	54.9	3612	23	US-11-524-707-973	Sequence 973, App
	24	2467.2	54.9	3612	23	US-11-524-787-973	Sequence 973, App
	25	2467.2	54.9	3612	23	US-11-524-790-973	Sequence 973, App
	26	2467.2	54.9	3612	23	US-11-524-791-973	Sequence 973, App
	27	2467.2	54.9	3612	23	US-11-524-833-973	Sequence 973, App
	28	2467.2	54.9	3612	23	US-11-524-942-973	Sequence 973, App
	29	2467.2	54.9	3612	23	US-11-524-943-973	Sequence 973, App
	30	2467.2	54.9	3612	23	US-11-524-354-973	Sequence 973, App
	31	2467.2	54.9	3612	23	US-11-028-169-973	Sequence 973, App
	32	2467.2	54.9	3612	23	US-11-524-746-973	Sequence 973, App
	33	2467.2	54.9	3612	25	US-11-524-164-973	Sequence 973, App
	34	2467.2	54.9	3612	25	US-11-524-355-973	Sequence 973, App
	35	2467.2	54.9	3612	25	US-11-607-618-973	Sequence 973, App
	36	2467.2	54.9	3612	25	US-11-607-689-973	Sequence 973, App
	37	2467.2	54.9	3612	26	US-11-643-458-973	Sequence 973, App
	38	2467.2	54.9	3612	26	US-11-643-289-973	Sequence 973, App
	39	2467.2	54.9	3612	26	US-11-643-532-973	Sequence 973, App
	40	2467.2	54.9	3612	26	US-11-643-556-973	Sequence 973, App
	41	2467.2	54.9	3612	26	US-11-607-413-973	Sequence 973, App
	42	2467.2	54.9	3612	27	US-11-643-463-973	Sequence 973, App
	43	2462.4	54.8	3609	10	US-10-472-928-4085	Sequence 4085, Ap
	44	2436.6	54.2	3567	22	US-11-348-413-1550	Sequence 1550, Ap
	45	2423.4	53.9	3567	9	US-10-282-122A-38159	Sequence 38159, A

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12 ; Search time 52 Seconds
                                        (without alignments)
                                        9152.710 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
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               11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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               22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18.8	100.0	20	14	US-10-529-319-6	Sequence 6, Appli
c	2	18.8	100.0	162	3	US-09-815-242-992	Sequence 992, App
c	3	18.8	100.0	162	9	US-10-282-122A-977	Sequence 977, App
c	4	18.8	100.0	456	3	US-09-815-242-3096	Sequence 3096, Ap
c	5	18.8	100.0	456	9	US-10-282-122A-5649	Sequence 5649, Ap
	6	18.8	100.0	763	9	US-10-398-221-1429	Sequence 1429, Ap
	7	18.8	100.0	891	11	US-10-750-185-42683	Sequence 42683, A
	8	18.8	100.0	891	11	US-10-750-623-42683	Sequence 42683, A
	9	18.8	100.0	891	15	US-10-750-622-42683	Sequence 42683, A
	10	18.8	100.0	2205	14	US-10-434-665-2197	Sequence 2197, Ap
	11	18.8	100.0	3096	14	US-10-529-319-5	Sequence 5, Appli
	12	18.8	100.0	3198	14	US-10-529-319-4	Sequence 4, Appli
	13	18.8	100.0	3405	9	US-10-282-122A-35573	Sequence 35573, A
	14	18.8	100.0	3411	3	US-09-815-242-8349	Sequence 8349, Ap
	15	18.8	100.0	3411	3	US-09-815-242-8716	Sequence 8716, Ap
	16	18.8	100.0	3425	14	US-10-529-319-3	Sequence 3, Appli
	17	18.8	100.0	3474	3	US-09-815-242-3939	Sequence 3939, Ap
	18	18.8	100.0	3537	3	US-09-815-242-4467	Sequence 4467, Ap
	19	18.8	100.0	3549	10	US-10-470-048B-125	Sequence 125, App
	20	18.8	100.0	3549	13	US-10-471-571A-3397	Sequence 3397, Ap
	21	18.8	100.0	3552	9	US-10-282-122A-7607	Sequence 7607, Ap
	22	18.8	100.0	3552	10	US-10-857-625-235	Sequence 235, App
	23	18.8	100.0	3552	15	US-10-859-198-1712	Sequence 1712, Ap
	24	18.8	100.0	3552	15	US-10-859-198-9564	Sequence 9564, Ap
	25	18.8	100.0	3555	9	US-10-282-122A-24519	Sequence 24519, A
	26	18.8	100.0	3561	9	US-10-282-122A-36012	Sequence 36012, A
	27	18.8	100.0	3564	22	US-11-434-137-379	Sequence 379, App
	28	18.8	100.0	3564	22	US-11-434-184-379	Sequence 379, App
	29	18.8	100.0	3564	22	US-11-434-199-379	Sequence 379, App
	30	18.8	100.0	3564	22	US-11-434-203-379	Sequence 379, App
	31	18.8	100.0	3564	22	US-11-434-127-379	Sequence 379, App
	32	18.8	100.0	3567	9	US-10-282-122A-38159	Sequence 38159, A
	33	18.8	100.0	3567	14	US-10-513-024-723	Sequence 723, App
	34	18.8	100.0	3567	22	US-11-348-413-1550	Sequence 1550, Ap
	35	18.8	100.0	3578	3	US-09-974-300-1310	Sequence 1310, Ap
	36	18.8	100.0	3578	23	US-11-203-606-1310	Sequence 1310, Ap
	37	18.8	100.0	3579	11	US-10-498-302-1	Sequence 1, Appli
	38	18.8	100.0	3582	8	US-10-369-493-46739	Sequence 46739, A
	39	18.8	100.0	3591	8	US-10-369-493-42178	Sequence 42178, A
	40	18.8	100.0	3612	9	US-10-282-122A-6253	Sequence 6253, Ap
	41	18.8	100.0	3624	3	US-09-815-242-6529	Sequence 6529, Ap
	42	18.8	100.0	3624	9	US-10-282-122A-21771	Sequence 21771, A
	43	18.8	100.0	3698	10	US-10-488-588-5	Sequence 5, Appli
	44	18.8	100.0	3791	10	US-10-488-588-3	Sequence 3, Appli
	45	18.8	100.0	3851	10	US-10-488-588-6	Sequence 6, Appli

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12 ; Search time 60 Seconds
                                          (without alignments)
                                          9152.710 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
            1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*
            2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22.2	100.0	23	14	US-10-529-319-7	Sequence 7, Appli
	2	22.2	100.0	23	14	US-10-529-319-49	Sequence 49, Appl
	3	22.2	100.0	158	3	US-09-815-242-474	Sequence 474, App
	4	22.2	100.0	158	3	US-09-815-242-2058	Sequence 2058, Ap
	5	22.2	100.0	158	9	US-10-282-122A-488	Sequence 488, App
	6	22.2	100.0	158	9	US-10-282-122A-4567	Sequence 4567, Ap
	7	22.2	100.0	166	3	US-09-815-242-3017	Sequence 3017, Ap
	8	22.2	100.0	166	3	US-09-815-242-3348	Sequence 3348, Ap
	9	22.2	100.0	166	9	US-10-282-122A-5591	Sequence 5591, Ap
	10	22.2	100.0	166	9	US-10-282-122A-5936	Sequence 5936, Ap
	11	22.2	100.0	202	3	US-09-815-242-2351	Sequence 2351, Ap
	12	22.2	100.0	202	9	US-10-282-122A-4862	Sequence 4862, Ap
c	13	22.2	100.0	271	2	US-08-781-986A-4462	Sequence 4462, Ap
c	14	22.2	100.0	271	9	US-10-329-624-4462	Sequence 4462, Ap
c	15	22.2	100.0	271	14	US-10-807-556-4462	Sequence 4462, Ap
	16	22.2	100.0	274	3	US-09-815-242-368	Sequence 368, App
	17	22.2	100.0	274	3	US-09-815-242-567	Sequence 567, App
	18	22.2	100.0	274	9	US-10-282-122A-386	Sequence 386, App
	19	22.2	100.0	274	9	US-10-282-122A-559	Sequence 559, App
	20	22.2	100.0	275	3	US-09-815-242-442	Sequence 442, App
	21	22.2	100.0	275	9	US-10-282-122A-417	Sequence 417, App
	22	22.2	100.0	321	3	US-09-815-242-88	Sequence 88, Appl
	23	22.2	100.0	321	9	US-10-282-122A-82	Sequence 82, Appl
	24	22.2	100.0	400	2	US-08-781-986A-4154	Sequence 4154, Ap
	25	22.2	100.0	400	9	US-10-329-624-4154	Sequence 4154, Ap
	26	22.2	100.0	400	14	US-10-807-556-4154	Sequence 4154, Ap
	27	22.2	100.0	1546	9	US-10-398-221-1956	Sequence 1956, Ap
c	28	22.2	100.0	2205	14	US-10-434-665-2197	Sequence 2197, Ap
c	29	22.2	100.0	3096	14	US-10-529-319-5	Sequence 5, Appli
c	30	22.2	100.0	3411	3	US-09-815-242-8349	Sequence 8349, Ap
c	31	22.2	100.0	3411	3	US-09-815-242-8716	Sequence 8716, Ap
c	32	22.2	100.0	3474	3	US-09-815-242-3939	Sequence 3939, Ap
c	33	22.2	100.0	3537	3	US-09-815-242-4467	Sequence 4467, Ap
c	34	22.2	100.0	3549	10	US-10-470-048B-125	Sequence 125, App
c	35	22.2	100.0	3549	13	US-10-471-571A-3397	Sequence 3397, Ap
c	36	22.2	100.0	3552	9	US-10-282-122A-7607	Sequence 7607, Ap
c	37	22.2	100.0	3552	10	US-10-857-625-235	Sequence 235, App
c	38	22.2	100.0	3552	15	US-10-859-198-1712	Sequence 1712, Ap
c	39	22.2	100.0	3552	15	US-10-859-198-9564	Sequence 9564, Ap
c	40	22.2	100.0	3555	9	US-10-282-122A-24519	Sequence 24519, A
c	41	22.2	100.0	3561	9	US-10-282-122A-36012	Sequence 36012, A
c	42	22.2	100.0	3564	22	US-11-434-137-379	Sequence 379, App
c	43	22.2	100.0	3564	22	US-11-434-184-379	Sequence 379, App
c	44	22.2	100.0	3564	22	US-11-434-199-379	Sequence 379, App
c	45	22.2	100.0	3564	22	US-11-434-203-379	Sequence 379, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12 ; Search time 1838 Seconds
                                        (without alignments)
                                        9152.710 Million cell updates/sec

Title: US-10-529-319-8
Perfect score: 709
Sequence: 1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709

Scoring table: IDENTITY_NUCDX
                  Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
            1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_PUBCOMB.seq:*
            2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_PUBCOMB.seq:*
            3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
            4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
            5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
            6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
            7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
            8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
            9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
           10: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
           11: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
           12: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
           13: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
           14: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
           15: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
           16: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
           17: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10K_PUBCOMB.seq:*
           18: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
           19: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11B_PUBCOMB.seq:*
           20: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11C_PUBCOMB.seq:*
           21: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11D_PUBCOMB.seq:*
           22: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
           23: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11F_PUBCOMB.seq:*
           24: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11G_PUBCOMB.seq:*
           25: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11H_PUBCOMB.seq:*
           26: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11I_PUBCOMB.seq:*
           27: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11J_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	709	100.0	709	14	US-10-529-319-8	Sequence 8, Appli
	2	619	87.3	4118	14	US-10-529-319-2	Sequence 2, Appli
c	3	593.8	83.8	728	14	US-10-529-319-21	Sequence 21, Appl
	4	568.2	80.1	3471	3	US-09-815-242-9089	Sequence 9089, Ap
	5	568.2	80.1	3651	9	US-10-282-122A-37985	Sequence 37985, A
	6	566.6	79.9	3612	23	US-11-027-802-973	Sequence 973, App
	7	566.6	79.9	3612	23	US-11-027-892-973	Sequence 973, App
	8	566.6	79.9	3612	23	US-11-028-050-973	Sequence 973, App
	9	566.6	79.9	3612	23	US-11-028-149-973	Sequence 973, App
	10	566.6	79.9	3612	23	US-11-028-197-973	Sequence 973, App
	11	566.6	79.9	3612	23	US-11-028-204-973	Sequence 973, App
	12	566.6	79.9	3612	23	US-11-028-458-973	Sequence 973, App
	13	566.6	79.9	3612	23	US-11-524-439-973	Sequence 973, App
	14	566.6	79.9	3612	23	US-11-524-493-973	Sequence 973, App
	15	566.6	79.9	3612	23	US-11-524-707-973	Sequence 973, App
	16	566.6	79.9	3612	23	US-11-524-787-973	Sequence 973, App
	17	566.6	79.9	3612	23	US-11-524-790-973	Sequence 973, App
	18	566.6	79.9	3612	23	US-11-524-791-973	Sequence 973, App
	19	566.6	79.9	3612	23	US-11-524-833-973	Sequence 973, App
	20	566.6	79.9	3612	23	US-11-524-942-973	Sequence 973, App
	21	566.6	79.9	3612	23	US-11-524-943-973	Sequence 973, App
	22	566.6	79.9	3612	23	US-11-524-354-973	Sequence 973, App
	23	566.6	79.9	3612	23	US-11-028-169-973	Sequence 973, App
	24	566.6	79.9	3612	23	US-11-524-746-973	Sequence 973, App
	25	566.6	79.9	3612	25	US-11-524-164-973	Sequence 973, App
	26	566.6	79.9	3612	25	US-11-524-355-973	Sequence 973, App
	27	566.6	79.9	3612	25	US-11-607-618-973	Sequence 973, App
	28	566.6	79.9	3612	25	US-11-607-689-973	Sequence 973, App
	29	566.6	79.9	3612	26	US-11-643-458-973	Sequence 973, App
	30	566.6	79.9	3612	26	US-11-643-289-973	Sequence 973, App
	31	566.6	79.9	3612	26	US-11-643-532-973	Sequence 973, App
	32	566.6	79.9	3612	26	US-11-643-556-973	Sequence 973, App
	33	566.6	79.9	3612	26	US-11-607-413-973	Sequence 973, App
	34	566.6	79.9	3612	27	US-11-643-463-973	Sequence 973, App
	35	566.6	79.9	3651	11	US-10-617-320-1652	Sequence 1652, Ap
	36	563.4	79.5	3609	10	US-10-472-928-4085	Sequence 4085, Ap
c	37	563.4	79.5	14672	2	US-08-961-527-111	Sequence 111, App
c	38	563.4	79.5	14672	9	US-10-158-844-111	Sequence 111, App
c	39	563.4	79.5	14672	27	US-11-563-552-111	Sequence 111, App
c	40	563.4	79.5	2162598	10	US-10-472-928-4979	Sequence 4979, Ap
c	41	561	79.1	728	14	US-10-529-319-10	Sequence 10, Appl
c	42	555.4	78.3	728	14	US-10-529-319-19	Sequence 19, Appl
c	43	553	78.0	725	14	US-10-529-319-9	Sequence 9, Appli
	44	546.6	77.1	3576	22	US-11-348-413-6399	Sequence 6399, Ap
c	45	545.8	77.0	714	14	US-10-529-319-23	Sequence 23, Appl

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45 ; Search time 1155 Seconds
                                          (without alignments)
                                          2488.446 Million cell updates/sec

Title: US-10-529-319-1
Perfect score: 4494.2
Sequence: 1 tcatacttttagagtcagat..........tcaccgctcattccagacac 4523

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

                        %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
      1   2467.2   54.9   3612   7   US-11-803-079-973   Sequence 973, App
      2   2467.2   54.9   3612   7   US-11-803-173-973   Sequence 973, App
      3   2467.2   54.9   3612   8   US-11-796-730-973   Sequence 973, App
      4   455.6   10.1   3678   7   US-11-803-079-976   Sequence 976, App
      5   455.6   10.1   3678   7   US-11-803-173-976   Sequence 976, App
      6   455.6   10.1   3678   8   US-11-796-730-976   Sequence 976, App
      7   411   9.1 2242716   7   US-11-711-740-1   Sequence 1, Appli
c   8   234.4   5.2   348   7   US-11-803-079-974   Sequence 974, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45 ; Search time 5 Seconds
                                            (without alignments)
                                            2488.446 Million cell updates/sec

Title: US-10-529-319-6
Perfect score: 18.8
Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB ID   Description
----
c   1   17.8   94.7   1153   8   US-11-514-704-10707   Sequence 10707, A
c   2   17.8   94.7   2488   8   US-11-514-704-10710   Sequence 10710, A
c   3   17.6   93.6   348   7   US-11-803-079-974   Sequence 974, App
c   4   17.6   93.6   348   7   US-11-803-173-974   Sequence 974, App
c   5   17.6   93.6   348   8   US-11-796-730-974   Sequence 974, App
     6   17.6   93.6   3612   7   US-11-803-079-973   Sequence 973, App
     7   17.6   93.6   3612   7   US-11-803-173-973   Sequence 973, App
     8   17.6   93.6   3612   8   US-11-796-730-973   Sequence 973, App

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45 ; Search time 6 Seconds
                                        (without alignments)
                                        2488.446 Million cell updates/sec

Title: US-10-529-319-7
Perfect score: 22.2
Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

            %
Result   Query
    No.   Score Match Length DB   ID   Description
----
 c 1   20.6   92.8   3612 7   US-11-803-079-973   Sequence 973, App
 c 2   20.6   92.8   3612 7   US-11-803-173-973   Sequence 973, App
 c 3   20.6   92.8   3612 8   US-11-796-730-973   Sequence 973, App
    4   18   81.1   681 6   US-10-529-351A-3924   Sequence 3924, Ap
 c 5   18   81.1   1486 6   US-10-438-246-4308   Sequence 4308, Ap
 c 6   17.8   80.2   1562 8   US-11-514-704-13511   Sequence 13511, A
    7   17.8   80.2 169659 7   US-11-403-116-1165   Sequence 1165, Ap
    8   17.4   78.4   336 7   US-11-239-610A-39312   Sequence 39312, A

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45 ; Search time 181 Seconds
                                  (without alignments)
                                  2488.446 Million cell updates/sec

Title: US-10-529-319-8
Perfect score: 709
Sequence: 1 cgcgaaattccaaacgttgg..........tcaccacatggttgatgaca 709

Scoring table: IDENTITY_NUCDX
                 Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_New:*
                 1: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                 2: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 5: /EMC_Celerra_SIDS2/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 6: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                 7: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                 8: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                 9: /EMC_Celerra_SIDS2/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	566.6	79.9	3612	7	US-11-803-079-973	Sequence 973, App
2	566.6	79.9	3612	7	US-11-803-173-973	Sequence 973, App
3	566.6	79.9	3612	8	US-11-796-730-973	Sequence 973, App
c 4	234	33.0	348	7	US-11-803-079-974	Sequence 974, App
c 5	234	33.0	348	7	US-11-803-173-974	Sequence 974, App
c 6	234	33.0	348	8	US-11-796-730-974	Sequence 974, App
7	130.4	18.4	2242716	7	US-11-711-740-1	Sequence 1, Appli
8	66	9.3	1562	8	US-11-514-704-13511	Sequence 13511, A